

APPROVED BY DRAFTSMAN	O.G. FIG.
	CLASS SUBCLASS

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1

ATC TTTGTTCA GT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTGGATGTA 93

94 TGTCTTGGC AGGATGATAA AGAACAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153

154 AGGCTGTGTC TGCTCTTATT TTGAGTGCAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213

214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273

274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACCTTTCC 333

334 CTTTGTCCCC AATTCAGGA AAAATGATG AGGACCAAAA TCAATGAATA AGGAAAACAG 393
(Pr1.FPIII) CCTG AAAATGAATA AGAAA

394 CTCAGAAAAA AGATGTTTCC AAATGGTAA TTAAGTATTGTT GTTCTTGGG AAGAGACCTC 453
(PR/GR-MMTV) T GTTCTTTGG AA
(SSRE) GAGACC

454 CATGTGAGCT TGATGGAAA ATGGGAAAAA CGTCAAAGC ATGATCTGAT CAGATCCCA 513

514 AGTGGATTAT TATTTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573

574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633
CCTTTAG-A AAGGACAAAA CAGAATG (nGRE-PRL)

634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGAACACC 693

694 TCCCCGTCTA TACCAAGGAA CACAAAATT GACTGGCTA AGCCTGGACT TTCAAGGGAA 753
GCCTGGACT GTC (CBE-P53)

754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAAA GGCAACCAGA ACATTGTGAG 813
ATTTTCTGA TTGGTTAAAA GT (NFE1)

814 CCTTCAAAGC AGCAGTGCCTT CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873
G ACCCTGAGGC T (KTF.1-CS)

874 GTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTAACCC ATTTTAAGTA 933

934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGT CCCAATTTTA TAAAGTCAGG 993
(PRE-lysozyme) AGGCCGT

994 CATAACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTCAGAA ATCATTAGAA ATCACTGTGT 1053
GATCCAAGGA GCAGAAGTTC CAGCTATGGT CAG (GRE-hMT) GG TACACTGTGT

1054 CCCCATCCTA ACTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113
CCT

1114 TGACCTACAA CCACATCTAC AACCCAAGTG CCTCAACCAT TGTAAACGTG TCATCTCA 1173

FIG.1A

APPROVED	O.G. FIG.	
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FIG. 1B

APPROVED	O.G. FIG.	
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2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553
CTGG GGAGCCTGGG GA (AP.2-SV40)

2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTGTT TCACGGGGCT 2613

2614 GGGAGTTTC CGTTGCTTCC TGTGAGCCTT TTTATCTTT CTCTGCTTGG AGGAGAAGAA 2673
CT CGTTGCTTCG AG (HSTF-hsp70)

2674 GTCTATTC A TGAAGGGATG CAGTTCAT AAGTCAGCTG TTAAAATTCC AGGGTGTGCA 2733
A

2734 TGGGTTTCC TTCACGAAGG CCTTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTCCT 2793
TGGGTTTTG (SBF.yeast)

2794 AGGCCGTTAA TTCACGGAAG AAGTGACTGG AGTCTTTCT TTCAATGTCTT CTGGGCAACT 2853

2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTTGG AATCAGGAGA 2913

2914 CTCGGTTTC TTTCTGGTT TCGCCATTGGT TGGCTGTGCG ACCGTGGGCA AGTGTCTCTC 2973
C TTTCTGGTT TGCA (NF.1-bithorax)
(NF-MHCII/CCATTGGT T)

2974 CTTCCCTGGG CCATAGTC TTCTGCTATA AAGACCCCTG CAGCTCTCGT GTTCTGTGAA 3033

3034 CACTTCCCTG TGATTCTCTG TGAGGGGGGA TGTTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153

3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943

2944 CAATGAACCC AACAGCCACA TTTCCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273

3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTGCC TGGCATTCAA AACTGGGCC 3333
GAAGTGA CACTG (PEA.1-Polyoma)

3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTCAC CCTGACCAGC ACCCCACGCA 3393

3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453
C AGGTAGAGT GACCTG (ERE.2-Vitel.)

3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCTTCA AGGGCAGTGG GAATTGACCA 3513

3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573
(GRE-FLV) CGGGATAC CGAGAGAACAA GGGCTATAGG

3574 AAAATCAGTT CAAGGGAAAGT CGGGAGACCT GATTCTAAT ACTATATTT TCCTTACAA 3633
GAGACC (SSRE)

3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAACTGAGG CTGTAAGATT ACTTAGTTTC 3693
(ICS-MTII/ HLA-DR/)AGTTTC

3694 TCCTTATTAG GAACTCTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTCTT 3753
TCCTCT

3754 TTAACAGGAA GAAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813

3814 GACTATATGA TTGGTTTTT GAAAATCAT TTCAGCGATG TTTACTATCT GATTCAAGAAA 3873

FIG.1C

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3874 ATGAGACTAG TACCCCTTGG TCAGCTGTAA ACAAACACCC ATTTGAAAT GTCTCAAGTT 3933
GG TCA (1/2 ERE)

3934 CAGGCTTAAC TGCAGAACCA ATCAAATAAG AATAGAATCT TTAGAGCAA CTGTGTTCT 3993

3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTACTTCACA AGTATTGACA 4053

4054 CTGTTGTTGG TATTAACAAAC ATAAAGTTGC TCAAAGGCAA TCATTATTC AAGTGGCTTA 4113

4114 AAGTTACTTC TGACAGTTT GGTATATTAA TTGGCTATTG CCATTGCTT TTTGTTTTT 4173
(NF.1-HCMV) TTGGCTATTG GCCA CTTT

4174 CTCTTGGGT TTATTAATGT AAAGCAGGGA TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233
CTCTT (ISGF2)

4234 ATTTGAATGA GGAAAAAATT ACATTTTGT TTTTACCACC TTCTAACTAA ATTTAACATT 4293
(Zn binding)-----

4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAACAGTACC TGTGATTTG 4353

4354 TCATTACCAA TAGAAATCAC AGACATTTA TACTATATTAA CAGTTGTTGC AGATACGTTG 4413
(CAP-galO) ATTTA TTCCATGTCA CACTTTCGC A

4414 TAAGTGAAT ATTTATACAC AAAACTACTT TGAAATTAGA CCTCCTGCTG GATCTTGT 4473
TTACAC A (AP-1)

4474 TTAACATATT AATAAAACAT GTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533
GAT GTTAAAAT (PRL-FPII)

4534 ATTTGTTCC TTTGTAATCT ATATTTATA TATTTGAAAA CATCTTCTG AGAAGAGTTC 4593
(GRE-MuRFV) TGTTTTCTG AGAACATCAG

4594 CCCAGATTC ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTAGA 4653
CCAGATCTC ACCATCATTAT (nGRE) CACACACAC A (CACA)
CTCTGG GGACAC AGAGTAGGG (AP.1-TGFb)

4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713
(GC2) GATGCT GATGGATAAT TTAGAAGCTT CTCCCACA

4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTCTA TAGGAATGCT 4773
(PEA.3)AGGAA GGT

4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCTT GTGTTCTGGC TGGCTGTTAT TTTCTCTGT 4833
CTC (SSRE) MIR Repeat Region

4834 CCCTGCTACG TCTTAAAGGA CTTGTGGAA TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893
GGA CTTGTTGTT CT (GRE-rTAT-II) TGGGCACA
GCAAAAAGGA TCTATTTGGA A (GRE-MMTV)

4894 GTGCAGGTTTC TCAATGAGTT TGCGAGGTGA ATGGAAATAT AAACTAGAAA TATATCCTG 4953
GTGCCAA (NF-1) (HNF-1)C TGTGAAATAT TAACTAAA

4954 TTGAAATCAG CACACCAGTA GTCTGGTGT AAGTGTGTGT ACGTGTGTGT GTGTGTGT 5013

FIG.1D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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5014 GTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5073
cat/reverse cat box

5074 TGGGATGTTC TTTTTAAAAA GAAACTCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5133
(1/2GRE)TGTTC T (HSTF) GAAACTTCT GGAATATTCC CGAACTTTC
C CTTTAGAAA GGA---CAA ACAGAATG(nGRE-Pr1)

5134 TCTTGCTGGC AGCGTGAAGG CAACCCCCCT GTGCACAGCC CCACCCAGCC TCACGTGCC 5193
(1/2 TRE)AGG CAA T-CC CCAGGCTCCC -CAG(AP.2-SV40)
GGAGAGCC CC (NF-KB)

5194 ACCTCTGTCT TCCCCATGA AGGGCTGGCT CCCCAGTATA TATAAACCTC TCTGGAGCTC 5253
tata box GGTC TC (SSRE)

5254 GGGCATGAGC CAGCAAGGC*C* ACCCATCCAG GCACCTCTCA GCACAGC 5300
Start Sites

FIG.1E

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ATC TTTGTTCA GT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTGGATGTA 93
 94 TGTCTTGGC AGGATGATAA AGAACAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153
 154 AGGCTGTGTC TGCTCTTATT TTAGTGACAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213
 214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273
 274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACTTTCC 333
 334 CTTTGTTTT AATTCAGGA AAAAATGATG AGGACCAAAA TCAATGAATA AGGAAAACAG 393
 394 CTCAGAAAAA AGATGTTCC AAATTGGTAA TTAAGTATTT GTTCCCTGGG AAGAGACCTC 453
 454 CATGTGAGCT TGATGGAAA ATGGGAAAA CGTCAAAAGC ATGATCTGAT CAGATCCAA 513
 514 AGTGGATTAT TATTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573
 574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633
 634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGAACACC 693
 694 TCCCCGTCTA TACCAGGGAA CACAAAATT GACTGGCTA AGCCTGGACT TTCAAGGGAA 753
 754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAAA GGCAACCAGA ACATTGTGAG 813
 814 CCTTCAAAGC AGCAGTGCCC CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873
 874 GTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTAACCC ATTTTAAGTA 933
 934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGGT CCCAATTTA TAAAGTCAGG 993
 994 CATAACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTCAAGAA ATCATTAGAA ATCACTGTGT 1053
 1054 CCCCATCCTA ACTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113
 1114 TGACCTACAA CCACATCTAC AACCCAAAGTG CCTCAACCCT TGTTAACGTG TCATCTCAGT 1173
 1174 AGGTCCCATT ACAAAATGCCA CCTCCCCGTG GCAGCCCATC CCGCTCCACA GGAAGTCTCC 1233
 1234 CCACTCTAGA CTTCTGCATC ACGATGTTAC AGCCAGAAGC TCCGTGAGGG TGAGGGTCTG 1293
 1294 TGTCTTACAC CTACCTGTAT GCTCTACACC TGAGCTCACT GCAACCTCTG CCTCCCAGGT 1353
 1354 TCAAGCAATT CTCCTGTCTC AGCCTCCCGC GTAGCTGGGA CTACAGGCGC ACGCCCGGCT 1413
 1414 AATTTTGTA TTGTTAGTAG AGATGGGGTT TCACCATATT AGCCCGGCTG GTCTTGAAC 1473

FIG.2A

APPROVED	O.G. FIG.	
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1474 CCTGACCTCA GGTGATCCAC CCACCTCAGC CTCCTAAAGT GCTGGGATTA CAGGCATGAG 1533
 1534 TCACCGCGCC CGGCCAAGGG TCAGTGTAA ATAAGGAATA ACTTGAATGG TTTACTAAAC 1593
 1594 CAACAGGGAA ACAGACAAAA GCTGTGATAA TTTCAGGGAT TCTTGGGATG GGGATGGTG 1653
 1654 CCATGAGCTG CCTGCCTAGT CCCAGACCAC TGGTCCTCAT CACTTCTTC CCTCATCCTC 1713
 1714 ATTTTCAGGC TAAGTTACCA TTTTATTACAC CATGCTTTG TGGTAAGCCT CCACATCGTT 1773
 1774 ACTGAAATAA GAGTATACAT AACTAGTTC CATTGGGGC CATCTGTGTG TGTGTATAGG 1833
 1834 GGAGGAGGGC ATACCCCAGA GACTCCTGA AGCCCCGGC AGAGGTTTC TCTCCAGCTG 1893
 1894 GGGGAGCCCT GCAAGCACCC GGGGTCTGG GTGTCTGAG CAACCTGCCA GCCCGTGCCA 1953
 1954 CTGGTTGTT TGTTATCACT CTCTAGGGAC CTGTTGCTTT CTATTTCTGT GTGACTCGTT 2013
 2014 CATTCACTCCA GGCATTCATT GACAATTAT TGAGTACTTA TATCTGCCAG ACACCAGAGA 2073
 2074 CAAAATGGTG AGCAAAGCAG TCACTGCCCT ACCTTCGTGG AGGTGACAGT TTCTCATGGA 2133
 2134 AGACGTGCAG AAGAAAATTA ATAGCCAGCC AACTTAAACC CAGTGCTGAA AGAAAGGAAA 2193
 2194 TAAACACCAT CTTGAAGAAT TGTGCGCAGC ATCCCTTAAC AAGGCCACCT CCCTAGCGCC 2253
 2254 CCCTGCTGCC TCCATCGTGC CCGGAGGCC CCAAGCCGA GTCTTCCAAG CCTCCTCCTC 2313
 2314 CATCAGTCAC AGCGCTGCAG CTGGCCTGCC TCGCTTCCCG TGAATCGTCC TGGTGCATCT 2373
 2374 GAGCTGGAGA CTCCTGGCT CCAGGCTCCA GAAAGGAAAT GGAGAGGGAA ACTAGTCTAA 2433
 2434 CGGAGAATCT GGAGGGGACA GTGTTCTC AGAGGGAAAG GGGCCTCCAC GTCCAGGAGA 2493
 2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553
 2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTGTT GTACGGGGCT 2613
 2614 GGGAGTTTC CGTTGCTTCC TGTGAGCCTT TTTATCTTT CTCTGCTTGG AGGAGAAGAA 2673
 2674 GTCTATTCA TGAAGGGATG CAGTTTCATA AAGTCAGCTG TAAATTCC AGGGTGTGCA 2733
 2734 TGGGTTTCC TTCACGAAGG CCTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTTCT 2793
 2794 AGGCCGTTAA TTCACGGAAG AAGTGAATGG AGTCTTTCT TTCATGTCTT CTGGGCAACT 2853
 2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTGG AATCAGGAGA 2913
 2914 CTCGGTTTC TTTCTGGTTC TGCCATTGGT TGGCTGTGCG ACCGTGGCA AGTGTCTCTC 2973
 2974 CTTCCCTGGG CCATAGTCTT CTCTGCTATA AAGACCCCTG CAGCTCTCGT GTTCTGTGAA 3033
 3034 CACTCCCTG TGATTCTCTG TGAGGGGGGA TGTTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

FIG.2B

APPROVED	O.G. FIG.	
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3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153
 3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943
 2944 CAATGAACCC AACAGCCCACA TTTTCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273
 3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTGCC TGGCATTCAA AAACCTGGCC 3333
 3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTCAC CCTGACCAGC ACCCCACGCA 3393
 3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453
 3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCAATTCA AGGGCAGTGG GAATTGACCA 3513
 3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573
 3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTCTAAT ACTATATTTT TCCTTACAA 3633
 3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAACTGAGG CTGTAAGATT ACTTAGTTTC 3693
 3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTCTT 3753
 3754 TTAACAGGAA GAAAACATTG CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813
 3814 GACTATATGA TTGGTTTTT GAAAATCAT TTCAGCGATG TTTACTATCT GATTGAGAAA 3873
 3874 ATGAGACTAG TACCCCTTGG TCAGCTGTA ACAAACACCC ATTTGTAAT GTCTCAAGTT 3933
 3934 CAGGCTTAAC TGCAAGACCA ATCAAATAAG AATAGAATCT TTAGAGCAAA CTGTGTTCT 3993
 3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTACTTCACA AGTATTGACA 4053
 4054 CTGTTGTTGG TATTAACAAC ATAAAGTTGC TCAAAGGCAA TCATTATTTA AAGTGGCTTA 4113
 4114 AAGTTACTTC TGACAGTTTT GGTATATTAA TTGGCTATTG CCATTTGCTT TTTGTTTTT 4173
 4174 CTCTTGGGT TTATTAATGT AAAGCAGGGG TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233
 4234 ATTTGAATGA GGAAAAAATT ACGTTTTAT TTTTACCAACC TTCTAACTAA ATTTAACATT 4293
 4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAAGAGTACC TGTGATTTG 4353
 4354 TCATTACCAA TAGAAATCAC AGACATTITA TACTATATTA CAGTTGTTGC AGGTACGTTG 4413
 4414 TAAGTGAAT ATTTATACTC AAAACTACTT TGAAATTAGA CCTCCTGCTG GATCTGTTT 4473
 4474 TTAACATATT AATAAAACAT GTTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533
 4534 ATTTGTTTCC TTTGTAATCT ATATTTATA TATTGAAAA CATCTTCTG AGAAGAGTTC 4593
 4594 CCCAGATTTC ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTAGA 4653
 4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713

FIG.2C

APPROVED	O.G. FIG.	
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4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTTCTA TAGGAATGCT 4773
4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCCTT GTGTTCTGGC TGGCTGTTAT TTTCTCTGT 4833
4834 CCCTGCTACG TCTTAAAGGA CTTGTTTGGA TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893
4894 GTGCAGGTTTC TCAATGAGTT TGCAAGGTGA ATGGAAATAT AACTAGAAA TATATCTTG 4953
4954 TTGAAATCAG CACACCAGTA GTCCTGGTGT AAGTGTGTGT ACGTGTGTGTGT GTGTGTGTGT5017
5018 GTGTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5077
5078 TGGGATGTTCTTTTAAAAA GAAACTCCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5137
5138 TCTTGCTGGC AGCGTGAAGG CAACCCCCCT GTGCACAGCC CCACCCAGCC TCACGTGGCC 5197
5198 ACCTCTGTCT TCCCCCATGA AGGGCTGGCT CCCCAGTATA TATAAACCTC TCTGGAGCTC 5257
5258 GGGCATGAGC CAGCAAGGCC ACCCATCCAG GCACCTCTCA GCACAGC 5304

FIG.2D

APPROVED	O.G. FIG.	
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1 ATCTTGTTG AGTTTACCTC AGGGCTATTG TGAAATGAAA TGAGATAACC
 51 AATGTGAAAG TCCTATAAAC TGTATAGCCT CCATTCGGAT GTATGTCTT
 101 GGCAGGATGA TAAAGAATCA GGAAGAAGGA GTATCCACGT TAGCCAAGTG
 151 TCCAGGCTGT GTCTGCTCTT ATTTTAGTGA CAGATGTTGC TCCTGACAGA
 201 AGCTATTCTT CAGGAAACAT CACATCCAAT ATGGTAAATC CATCAAACAG
 251 GAGCTAAGAA ACAGGAATGA GATGGGCACT TGCCCAAGGA AAAATGCCAG
 301 GAGAGCAAAT AATGATGAAA AATAAACTTT TCCCTTGTT TTTAATTCA
 351 GGAAAAAAATG ATGAGGACCA AAATCAATGA ATAAGGAAAA CAGCTCAGAA
 401 AAAAGATGTT TCCAAATTGG TAATTAAGTA TTTGTTCCCTT GGGAAAGAGAC
 451 CTCCATGTGA GCTTGATGGG AAAATGGGAA AAACGTCAAAGCAGATGATCT
 501 GATCAGATCC CAAAGTGGAT TATTATTTA AAAACCAGAT GGCATCACTC
 551 TGGGGAGGCA AGTCAGGAA GGTCAATGTTA GCAAAGGACA TAACAATAAC
 601 AGCAAAATCA AAATTCCGCA AATGCAGGAG GAAAATGGGG ACTGGGAAAG
 651 CTTTCATAAC AGTGATTAGG CAGTTGACCA TGTTGCAAC ACCTCCCCGT
 701 CTATACCAGG GAACACAAAA ATTGACTGGG CTAAGCCTGG ACTTTCAAGG
 751 GAAATATGAA AACTGAGAG CAAAACAAAA GACATGGTTA AAAGGCAACC
 801 AGAACATTGT GAGCCTCAA AGCAGCAGTG CCCCTCAGCA GGGACCCTGA
 851 GGCATTTGCC TTTAGGAAGG CCAGTTTCT TAAGGAATCT TAAGAAACTC
 901 TTGAAAGATC ATGAATTAA ACCATTTAA GTATAAAACA AATATGCGAT
 951 GCATAATCAG TTTAGACATG GGTCCAATT TTATAAAGTC AGGCATACAA
 1001 GGATAACGTG TCCCAGCTCC GGATAGGTCA GAAATCATTA GAAATCACTG
 1051 TGTCCCCATC CTAACCTTTT CAGAATGATC TGTCATAGCC CTCACACACA
 1101 GGCCCGATGT GTCTGACCTA CAACCACATC TACAACCCAA GTGCCTCAAC
 1151 CATTGTTAAC GTGTCATCTC AGTAGGTCCC ATTACAAATG CCACCTCCCC
 1201 TGTGCAGCCC ATCCCGCTCC ACAGGAAGTC TCCCCACTCT AGACTTCTGC
 1251 ATCACGATGT TACAGCCAGA AGCTCCGTGA GGGTGAGGGT CTGTTGCTTA

FIG.3A

APPROVED	O.G. FIG.	
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1301 CACCTACCTG TATGCTCTAC ACCTGAGCTC ACTGCAACCT CTGCCCTCCA
 1351 GGTTCAAGCA ATTCTCCTGT CTCAGCCTCC CGCGTAGCTG GGACTACAGG
 1401 CGCACGCCCG GCTAATTTT GTATTGTTAG TAGAGATGGG GTTTCACCAT
 1451 ATTAGCCCGG CTGGTCTTGA ACTCCTGACC TCAGGTGATC CACCCACCTC
 1501 AGCCTCCTAA AGTGCTGGGA TTACAGGCAT GAGTCACCGC GCCCGGCCAA
 1551 GGGTCAGTGT TTAATAAGGA ATAACTTGAA TGGTTTACTA AACCAACAGG
 1601 GAAACAGACA AAAGCTGTGA TAATTCAGG GATTCTGGG ATGGGGAATG
 1651 GTGCCATGAG CTGCCTGCCT AGTCCCAGAC CACTGGTCCT CATCACTTTC
 1701 TTCCCTCATC CTCATTTCA GGCTAAGTTA CCATTTATT CACCATGCTT
 1751 TTGTGGTAAG CCTCCACATC GTTACTGAAA TAAGAGTATA CATAAACTAG
 1801 TTCCATTTGG GGCCATCTGT GTGTGTGTAT AGGGGAGGGAG GGCATACCCC
 1851 AGAGACTCCT TGAAGCCCCC GGCAGAGGTT TCCTCTCCAG CTGGGGGAGC
 1901 CCTGCAAGCA CCCGGGGTCC TGGGTGTCTT GAGCAACCTG CCAGCCGTG
 1951 CCACTGGTTG TTTTGTATC ACTCTCTAGG GACCTGTTGC TTTCTATTTC
 2001 TGTGTGACTC GTTCATTATC CCAGGCATTC ATTGACAATT TATTGAGTAC
 2051 TTATATCTGC CAGACACCAG AGACAAAATG GTGAGCAAAG CAGTCACTGC
 2101 CCTACCTTCG TGGAGGTGAC AGTTTCTCAT GGAAGACGTG CAGAAGAAAA
 2151 TTAATAGCCA GCCAACTTAA ACCCAGTGCT GAAAGAAAGG AAATAAACAC
 2201 CATCTTGAAG AATTGTGCGC AGCATCCCTT ACAAGGCCA CCTCCCTAGC
 2251 GCCCCCTGCT GCCTCCATCG TGCCCGGAGG CCCCCAAGCC CGAGTCTTCC
 2301 AAGCCTCTC CTCCATCAGT CACAGCGCTG CAGCTGGCCT GCCTCGCTTC
 2351 CCGTGAATCG TCCTGGTGCA TCTGAGCTGG AGACTCCTTG GCTCCAGGCT
 2401 CCAGAAAGGA AATGGAGAGG GAAACTAGTC TAACGGAGAA TCTGGAGGGG
 2451 ACAGTGTTC CTCAGAGGGA AAGGGGCCTC CACGTCCAGG AGAATTCCAG
 2501 GAGGTGGGGA CTGCAGGGAG TGGGGACGCT GGGGCTGAGC GGGTGCTGAA
 2551 AGGCAGGAAG GTGAAAAGGG CAAGGCTGAA GCTGCCAGA TGTTCAAGTGT
 2601 TGTTCACGGG GCTGGGAGTT TTCCGTTGCT TCCTGTGAGC CTTTTATCT

FIG.3B

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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2651 TTTCTCTGCT TGGAGGGAGAA GAAGTCTATT TCATGAAGGG ATGCAGTTTC
 2701 ATAAAGTCAG CTGTTAAAAT TCCAGGGTGT GCATGGGTTT TCCTTCACGA
 2751 AGGCCTTTAT TTAATGGAA TATAGGAAGC GAGCTCATT CCTAGGCCGT
 2801 TAATTACCGG AAGAAGTGAC TGGAGTCTTT TCTTCATGT CTTCTGGGCA
 2851 ACTACTCAGC CCTGTGGTGG ACTTGGCTTA TGCAAGACGG TCGAAAACCT
 2901 TGGAATCAGG AGACTCGGTT TTCTTCTGG TTCTGCCATT GGTTGGCTGT
 2951 GCGACCGTGG GCAAGTGTCT CTCCTCCCT GGGCCATAGT CTTCTCTGCT
 3001 ATAAAGACCC TTGCAGCTCT CGTGTCTGT GAACACTTCC CTGTGATTCT
 3051 CTGTGAGGGGG GGATGTTGAG AGGGGAAGGA GGCAGAGCTG GAGCAGCTGA
 3101 GCCACAGGGGG AGGTGGAGGG GGACAGGAAG GCAGGCAGAA GCTGGGTGCT
 3151 CCATCAGTCC TCACTGATCA CGTCAGACTC CAGGACCGAG AGCCACAATG
 3201 CTTCAGGAAA GCTCAATGAA CCCAACAGCC ACATTTCTT TCCCTAAGCA
 3251 TAGACAATGG CATTGCCAA TAACCAAAAA GAATGCAGAG ACTAACTGGT
 3301 GGTAGCTTTT GCCTGGCATT CAAAAACTGG GCCAGAGCAA GTGGAAAATG
 3351 CCAGAGATTG TTAAACTTTT CACCCCTGACC AGCACCCAC GCAGCTCAGC
 3401 AGTGAUTGCT GACAGCACGG AGTGAUTGC AGCGCAGGGG AGGAGAAGAA
 3451 AAAGAGAGGG ATAGTGTATG AGCAAGAAAG ACAGATTCA TCAAGGGCAG
 3501 TGGGAATTGA CCACAGGGAT TATAGTCCAC GTGATCCTGG GTTCTAGGAG
 3551 GCAGGGCTAT ATTGTGGGGG GAAAAAAATCA GTTCAAGGGAA AGTCGGGAGA
 3601 CCTGATTCT AATACTATAT TTTTCCTTA CAAGCTGAGT AATTCTGAGC
 3651 AAGTCACAAG GTAGTAUTG AGGCTGTAAAG ATTACTTAGT TTCTCCTTAT
 3701 TAGGAUTCT TTTCTCTGT GGAGTTAGCA GCACAAGGGC AATCCGTTT
 3751 CTTTAACAG GAAGAAAACA TTCCTAAGAG TAAAGCCAAA CAGATTCAAG
 3801 CCTAGGTCTT GCTGAUTATA TGATTGGTTT TTTGAAAAAT CATTTCAGCG
 3851 ATGTTTACTA TCTGATTCAAG AAAATGAGAC TAGTACCCCTT TGGTCAGCTG
 3901 TAAACAAACA CCCATTGTA AATGTCTCAA GTTCAGGGCTT AACTGCAGAA
 3951 CCAATCAAAT AAGAATAGAA TCTTAGAGC AACTGTGTT TCTCCACTCT

FIG.3C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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4001 GGAGGTGAGT CTGCCAGGGC AGTTTGGAAA TATTTACTTC ACAAGTATTG
 4051 ACACTGTTGT TGGTATTAAC AACATAAAGT TGCTCAAAGG CAATCATTAT
 4101 TTCAAGTGGC TTAAAGTTAC TTCTGACAGT TTTGGTATAT TTATTGGCTA
 4151 TTGCCATTG CTTTTGTTT TTTCTTTG GGTTTATTAA TGAAAGCAG
 4201 GGATTATTAA CCTACAGTCC AGAAAGCCTG TGAATTGAA TGAGGAAAAA
 4251 ATTACATTAA TGTTTTTACCC ACCTTCTAAC TAAATTAAAC ATTTTATTCC
 4301 ATTGCGAATA GAGCCATAAA CTCAAAGTGG TAATAACAGT ACCTGTGATT
 4351 TTGTCATTAC CAATAGAAAT CACAGACATT TTATACTATA TTACAGTTGT
 4401 TGCAGATACG TTGTAAGTGA AATATTATA CTCAAAACCA CTTGAAATT
 4451 AGACCTCCTG CTGGATCTTG TTTTAACAT ATTAATAAAA CATGTTAAA
 4501 ATTTGATAT TTTGATAATC ATATTCATT ATCATTGTT TCCTTGAA
 4551 TCTATATTAA ATATATTGA AAACATCTT CTGAGAAGAG TTCCCCAGAT
 4601 TTCACCAATG AGGTTCTGG CATGCACACA CACAGAGTAA GAACTGATT
 4651 AGAGGCTAAC ATTGACATTG GTGCCTGAGA TGCAAGACTG AAATTAGAAA
 4701 GTTCTCCCAA AGATACACAG TTGTTTAAA GCTAGGGGTG AGGGGGGAAA
 4751 TCTGCCGCTT CTATAGGAAT GCTCTCCCTG GAGCCTGGTA GGGTGCTGTC
 4801 CTTGTGTTCT GGCTGGCTGT TATTTTCTC TGTCCTGCT ACGTCTTAAA
 4851 GGACTTGTAA GGATCTCCAG TTCCCTAGCAT AGTGCCTGGC ACAGTGCAGG
 4901 TTCTCAATGA GTTGCAGAG TGAATGGAAA TATAAACTAG AAATATATCC
 4951 TTGTTGAAAT CAGCACACCA GTAGTCCTGG TGTAAGTGTG TGTACGTGTG
 5001 TGTGTGTGTG TGTGTGTGTG TGTAAAACCA GGTGGAGATA TAGGAACTAT
 5051 TATTGGGGTA TGGGTGCATA AATTGGGATG TTCTTTTAA AAAGAAACTC
 5101 CAAACAGACT TCTGGAAGGT TATTTCTAA GAATCTTGCT GGCAGCGTGA
 5151 AGGCAACCCC CCTGTGCACA GCCCCACCCA GCCTCACGTG GCCACCTCTG
 5201 TCTTCCCCCA TGAAGGGCTG GCTCCCCAGT ATATATAAAC CTCTCTGGAG
 5251 CTCGGGCATG AGCCAGCAAG GCCACCCATC CAGGCACCTC TCAGCACAGC 5300

FIG.3D

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

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1 AGAGCTTCCAGAGGAAGCCTCACCAAGCCTGCAATGAGGTTCTCTGTGCACGTTGC 60
 61 TGCAGCTTGGGCCTGAGATGCCAGCTGTCCAGCTGCTGCTCTGGCCTGCCTGGGTGG 120
 121 GATGTGGGGCCAGGACAGCTCAGTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180
 181 TATACCTTCAGTGTGCCAGTCCAATGAATCCAGCTGCCAGAGCAGAGCCAGGCCATG 240
 241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCAACGCTTAGACCTGGAGGCCACC 300
 301 AAAGCTCGACTCAGCTCCCTGGAGAGCCTCCTCACCAATTGACCTTGGACCAGGCTGCC 360
 361 AGGCCCCAGGAGACCCAGGAGGGGCTGCAGAGGGAGCTGGCACCCCTGAGGCGGGAGCGG 420
 421 GACCAGCTGGAAACCCAAACCAAGAGAGTTGGAGACTGCCTACAGCAACCTCCCTCCAGAC 480
 481 AAGTCAGTTCTGGAGGAAGAGAAGAAGCGACTAAGGAAGAAAATGAGAATCTGGCCAGG 540
 541 AGGTTGGAAAGCAGCAGCCAGGAGGTAGCAAGGCTGAGAAGGGGCCAGTGTCCCCAGACC 600
 601 CGAGACACTGCTCGGGCTGTGCCACCAGGCTCCAGAGAAG

(intron #1) gtaagaatgcagagtgggggactct
 gagttcagcaggtgatatggctcgtagtgacctgctacaggcgtccaggcctccctgccttctccta
 gagactgcacagctagcacaagacagatgaattaaggaaagcacaacgatcaccttcaagtattacta
 gtaatttagctcctgagagcttcattagatttagttggttcagagttcttgcgcctccatgtcag-----
 ----- Intron I ~10 Kb -----
 aaggttaggcacattgcctgcaatttataatttatgaggtgttcaattatggaattgtcaaattataaca
 aaagttagagagactacaatgaactccaatgttagccataactcaggcccaactgttatcagcacagtc
 aatcatgtttatcttcctctgacccccaacccatccccagtccttatctaaaatcaaattatcaaaca
 ccatactcttggagccattttatttagtttagtttagttcagacagagttcttcttgcgcctccaaagctgg
 agtacaatagtgtagtctcggtcaacagcaatctccctccctgggtcaagcaattctctgcctcagtc
 tcccaagaagctggattatagacacccgtccaccacatccagctaatttttgcgttttagaaaagaca
 gggttcaccatgtggccaggctgttgcactcctgcacccgtatccatgttgcgcctccatccca
 aagtgcggattacaggcatgagccaccacgcctggccggcagcctattaaatgtcatcctcaacat
 agtcaatccttggccattttctacagtaaaattttgtcttttttaatcag

(exon #2) TT TCT ACG TGG AAT TTG GAC

661 ACT TTG GCC TTC CAG GAACTG AAG TCC GAG CTA ACT GAAGTT CCT GCT TCC CGA ATT TTG 720
 721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGAG GAG GGA GAC ACCG

(intron #2)
 gtatgaagttaaatctccctttgtgcccacgtggctttattcatgtctagtgtgttgcagagaa
 tcagtataggtaaatgcccacccaaaggggaaattaactccctggagcagaggaggaggagg
 gaagaggaacagaactctctctctgttacccttgc----- Intron II ~ 3 kb -----

FIG.3E

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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tggctctgccaaggcttccgcatgatcatgtgtttggaaaggattatggattaaagtggcttcgtttt
cttctgttacacag

(exon #3) GA TGT GGA GAA CTA 780

781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840
841 GTG TGG ATG CGA GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900
901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960
961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CTC AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020
1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080
1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140
1141 TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200
1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260
1261 GAG AAT CTG GAA CTC GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320
1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC TAC ACC TCA GCA GAT GCT ACC 1380
1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC CCA TTC AAG 1440
1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG AAG CTC TTT GCC 1500
1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG

(3' flanking region) TGA AAA GCC TCC TCC 1560
1561 AAG CTG TAC AGG CAA TGG CAG AAG GAG ATG CTC AGG GCT CCT GGG GGG AGC AGG CTG AAG 1620
1621 GGA GAG CCA GCC AGC CAG GGC CCA GGC AGC ATG TAA CTC TAA CTA TCC AGG AAT TGT AGT TTT CCA AGT TTT CAT TAA TCC 1680
1681 AGA AGG ATG AAC ATG GTC ACC ATC TAA CTC TAA CTA TCC AGG AAT TGT AGT CTG AGG GCG TAG ACA 1740
1741 ATT TCA TAT AAT TAA TAT CCT TTA TCT TCT GTC AGC ATT TAT GGG ATG TTT AAT GAC ATA 1800
1801 GTT CAA GTT TTC TTG TGA TTT GGG GCA AAA GCT GTC AGG CAT AAT AGT CTT TTC CTG AAA 1860
1861 ACC ATT GCT CTT GCA TGT TAC ATG GTT ACC ACA AGC CAC AT AAT AAA AAG CAT AAC TTC TAA 1920
1921 AGG AAG CAG AAT AGC TCC TCT GGC CAG CAT CGA ATA TAA GAA ATT TAC TAC AGT 1980
1981 TGG CTT CTA ATG CTT CAG ATA GAA TAC AGT TGG GTC TCA CAT AAC CCT TAC ATT GTG AAA 2040
2041 TAA AAT TTT CTT ACC CAA CGT TCT CCT TGA ACT TTG TGG GAA TCT TTG CTT AAG AGA 2100
2101 AGG ATA TAG ATT CCA ACC ATC AGG TAA TTC CTT CAG GTT GGG AGA TGT GAT TGC AGG ATG 2160

FIG.3F

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
LAFTSMAN		

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2161 TTA AAG GTG TGT GTG TGT GTG TGT GTG TAA CTG AGA GGC TTG TGC CTG GTT TTG 2220
2221 AGG TGC TGC CCA GGA TGA CGC CAA GCA AAT AGC GCA TCC ACA CTT TCC CAC CTC CAT CTC 2280
2281 CTG GTG CTC TCG GCA CTA CGG GAG CAA TCT TTC CAT CTC TCC CCT GAA CCC ACC CTC TAT 2340
2341 TCA CCC TAA CTC CAC TTC AGT TTG ATT TTT TTT TTT TTT TTT TTT TGA 2400
2401 GAT GGG GTC TCG CTC TGT CAC CCA GGC TGG AGT GCA GTG GCA CGA TCT CGG CTC ACT GCA 2460
2461 AGT TCC GCC TCC CAG GTT CAC ACC ATT CTC CTG CCT CAG CCT CCC AAG TAG CTG GGA CTA 2520
2521 CAG GCA CCT GCC ACC ACG CCT GGC TAA TTT TTT TTT CCA GTG AAG ATG GGT TTC ACC 2580
2581 ATG TTA GCC AGG ATG GTC TCG ATC TCC TGAC CTT GTC ATC CAC CCA CCT TGG CCT CCC AAA 2640
2641 GTG CTG GGA TTA CAG GCG TGA GCC ACC ACGG CCA GCC CCT CCA CCT CAG TTT TTA TCT GTC 2700
2701 ATC AGG GGT ATG AAT TTT ATA AGC CAC ACC TCA GGT GGA GAA AGC TTG ATG CAT AGC TTG 2760
2761 AGT ATT CTA TAC TGT 2776

FIG. 3G

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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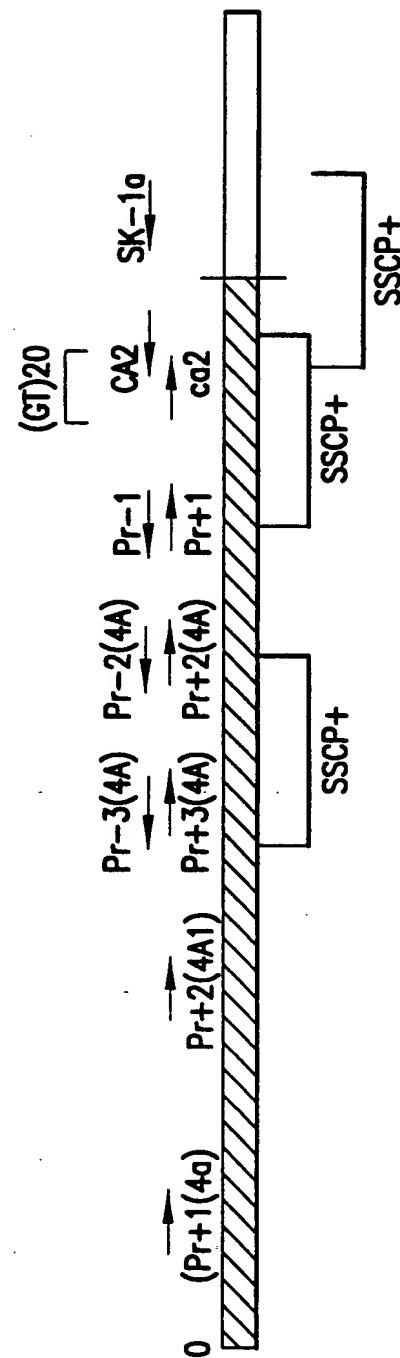


FIG.4

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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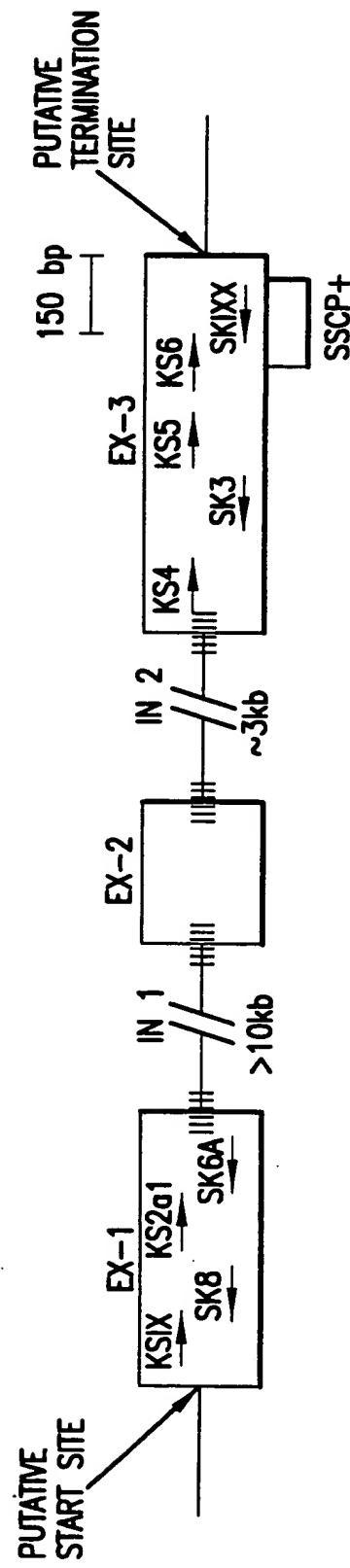


FIG.5

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

19/23

TIGR	-TGAVVYSGS	LYFQGAESRT	VIRYELNTET	VKAEEKIIPGA	GYHGQFPYSW	GGYTDIDLAV	59
ym08h12.r1	-----	-----	-----	--RFDLKTT	ILKTRSLDYA	GYNMNYHYAW	38
1B426bAMZ	GTGQVWYNGS	IYFNKFQSHI	IIRFDLKTT	ILKTRSLDYA	GYNMNYHYAW	GGHSDIDLW	60
ranofm	GAGVWWHNNN	LYYNCFNSHD	MCRASL-TSG	YVQKKPLLNA	LFNNRFSYAG	TMFQDMDFSS	59
Consensus	..G..VW....	.Y.....S...	..R..L..TETL..A	GYN...YAW	GG..DIDL..V	60

TIGR	DEAGLWVIYS	TDEAKGAIWL	SKLNPENL	EQTWETNIRK	QSVAANAFIIC	GTLYTVSSYT	119
ym08h12.r1	DESGLWAVYA	TNQNAGNIIV	SRLDPVSLQT	LQTWNTSYPK	RXPGXAFIIC	GTCYVVTNGY-	97
1B426bAMZ	DENGLWAVYA	TNQNAGNIIV	SKLDPVSLQI	LQTWNTSYPK	RSAGEAFIIC	GTLYVTNGYS	120
ranofm	DEKGLWVIIFT	TEKSAGKIVV	GKVNWATFTV	DNIWITTONQK	SDASNAFMIC	GVLVYTRSLG	119
Consensus	DE..GLW..Y.	T..AG..IV.	SKL..P..L..	QTW..T..K..	..AFIIC	GTLYVT..Y.	120

TIGR	SADATVNFAY	DTGTGISKTL	TIPFKNRKY	SSMIDYNPLE	KKLFAWDNLN	MVTYDIKLS	178
ym08h12.r1	SGGTKVHYAY	QTNAST---	-----	-----	NKLXP-----	--HFP-----	131
1B426bAMZ	GG-TKVHYAY	QTNASTYEYI	DIPFQNKYSH	ISMLDYNPKD	RALYAWNNGH	QTLYNVTLF	178
ranofm	PKMEEVFYMF	DTKTGKEGHL	SIMMEKMAEK	VHSLSYNSND	RKL YMFSEGY	LLHYDIAL-	177
ConsensusV.YAY	.T.....	.I.....Y..DYNP..	.KL.....Y..L..	178

FIG. 6

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

20/23

1 AGA GCT TTC CAG AGG AAG CCT CAC CAA GCC TCT GCA ATG AGG TTC TTC TGT GCA CGT TGC 60
 61 TGC AGC TTT GGG CCT GAG ATG CCA GCT GTC CAG CTG CTT CTG GCC CTG GTG TGG TGG 120
 121 GAT GTG GGG GCC AGG ACA GCT CAG CTC AGG AAG GCC AAT GAC CAG AGT GGC CGA TGC CAG 180
 181 TAT ACC TTC AGT GTG GCC AGT CCC AAT GAA TCC AGC TGC CCA GAG CAG AGC CAG GCC ATG 240
 241 TCA GTC ATC CAT AAC TTA CAG AGA GAC AGC AGC ACC CAA CGC TTA GAC CTG GAG GCC ACC 300
 301 AAA GCT CGA CTC AGC TCC CTG GAG AGC CTC CTC CAC CAA TTG ACC TTG GAC CAG GCT GCC 360
 361 AGG CCC CAG GAG ACC CAG GAG GGG CTG CAG AGG GAG CTG GGC ACC CTG AGG CGG GAG CGG 420
 421 GAC CAG CTG GAA ACC CAA ACC AGA GAG TTG GAG ACT GCC TAC AGC AAC CTC CTC CGA GAC 480
 481 AAG TCA GTT CTG GAG GAA GAG AAG CGA CTA AGG CAA GAA AAT GAG AAT CTG GCC AGG 540
 541 AGG TTG GAA AGC AGC AGC CAG GAG GCA AGG CTG AGA AGG GGC CAG TGT CCC CAG ACC 600
 601 CGA GAC ACT GCT CGG GCT GTG CCA CCA GGC TCC AGA GAA GTT TCT ACG TGG AAT TTG GAC 660
 661 ACT TTG GCC TTC CAG GAA CTG AAG TCC GAG CTA ACT GAA GTT CCT GCT TCC CGA ATT TTG 720
 721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG GGA GAC ACC GGA TGT GGA GAA CTA 780
 781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840
 841 GTG TGG ATG CGA GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900

FIG. 7A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960
 961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020
 1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080
 1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140
 1141 TTC CGG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200
 1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260
 1261 GAG AAT CTG GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320
 1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC 1380
 1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC ATC CCA TTC AAG 1440
 1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG CTC TTT GCC 1500
 1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG 1548

FIG. 7B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

22/23

1 Met Arg Phe Phe Cys Ala Arg Cys 20
21 Cys Ser Phe Gly Pro Glu Met Pro Ala Val Gln Leu Leu Ala Cys Leu Val Trp 40
41 Asp Val Gly Ala Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln 60
61 Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln Ser Gln Ala Met 80
81 Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr Gln Arg Leu Asp Leu Glu Ala Thr 100
101 Lys Ala Arg Leu Ser Ser Leu Glu Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala 120
121 Arg Pro Gln Glu Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg 140
141 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn Leu Leu Arg Asp 160
161 Lys Ser Val Leu Glu Glu Lys Lys Arg Leu Arg Gln Glu Asn Glu Asn Leu Ala Arg 180
181 Arg Leu Glu Ser Ser Ser Gln Glu Val Ala Arg Leu Arg Arg Gly Gln Cys Pro gln Thr 200
201 Arg Asp Thr Ala Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp 220
221 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala Ser Arg Ile Leu 240
241 Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu Gly Asp Thr Gly Cys Gly Glu Leu 260
261 Val Trp Val Gly Glu Pro Leu Thr Leu Arg Thr Ile Thr Gly Lys Tyr Gly 280
281 Val Trp Met Arg Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Trp Arg Ile 300

FIG. 8A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

23/23

301 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile Ser Gln Phe Met 320
 321 Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg Pro Leu Glu Ser Thr Gly Ala Val 340
 341 Val Tyr Ser Gly Ser Leu Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu 360
 361 Leu Asn Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gln Gly Ala Gly Tyr His Gln Gln 380
 381 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp Glu Ala Gly Leu 400
 401 Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala Ile Val Leu Ser Lys Leu Asn Pro 420
 421 Glu Asn Leu Glu Leu Glu Gln Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn 440
 441 Ala Phe Ile Ile Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr 460
 461 Val Asn Phe Ala Tyr Asp Thr Gly Thr Ile Ser Lys Thr Leu Thr Ile Pro Phe Lys 480
 481 Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn Pro Leu Glu Lys Lys Leu Phe Ala 500
 501 Trp Asp Asn Leu Asn Met Val Thr Tyr Asp Ile Lys Leu Ser Lys Met

FIG. 8B